

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: CORUZZI, GLORIA
LAM, HON-MING
HSIEH, MING-HSIUN

(ii) TITLE OF THE INVENTION: PLANT NITROGEN REGULATORY
P-PII GENES

(iii) NUMBER OF SEQUENCES: 21

(iv) CORRESPONDENCE ADDRESS:
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(C) CITY: New York
(D) STATE: NY
(E) COUNTRY: USA
(F) ZIP: 10036-2711

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 2.0

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/899,330
(B) FILING DATE: 23-JUL-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 60/022,328
(B) FILING DATE: 24-JUL-1996

(viii) ATTORNEY/AGENT INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Phe Tyr Lys Val Glu Ala Ile Val Arg Pro Trp Arg Ile Gln Gln Val
1 5 10 15
Ser Ser Ala Leu Leu Lys Ile Gly Ile Arg Gly Val Thr Val Ser Asp
20 25 30

Val Arg Gly Phe Gly Ala Gln Gly Gly Ser Thr Glu Arg His Gly Gly
35 40 45
Ser Glu Phe Ser Glu Asp Lys Phe Val Ala Lys Val Lys Met Glu Ile
50 55 60
Val Val Lys Lys Asp Gln Val Glu Ser Val Ile Asn Thr Ile Ile Glu
65 70 75 80
Gly Ala Arg Thr Gly Glu Ile Gly Asp Gly Lys Ile Phe Val Leu Pro
85 90 95
Val Ser Asp Val Ile Arg Val Arg Thr Gly Glu Arg Gly Glu Lys Ala
100 105 110
Glu

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Phe Tyr Lys Val Glu Ala Ile Leu Arg Pro Trp Arg Val Ser Gln Val
1 5 10 15
Ser Ser Ala Leu Leu Lys Ile Gly Ile Arg Gly Val Thr Val Ser Asp
20 25 30
Val Arg Gly Phe Gly Ala Gln Gly Gly Ser Thr Glu Arg Gln Gly Gly
35 40 45
Ser Glu Phe Ser Glu Asp Lys Phe Val Ala Lys Val Lys Met Glu Ile
50 55 60
Val Val Ser Lys Asp Gln Val Glu Asp Val Ile Glu Lys Ile Ile Glu
65 70 75 80
Glu Ala Arg Thr Gly Glu Ile Gly Asp Gly Lys Ile Phe Leu Leu Pro
85 90 95
Val Ser Asp Val Ile Arg Val Arg Thr Gly Glu Arg Gly Asp Lys Ala
100 105 110
Glu

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Lys Lys Ile Asp Ala Ile Ile Lys Pro Phe Lys Leu Asp Asp Val
1 5 10 15
Arg Glu Ala Leu Ala Glu Val Gly Ile Thr Gly Met Thr Val Thr Glu
20 25 30
Val Lys Gly Phe Gly Arg Gln Lys Gly His Thr Glu Leu Tyr Arg Gly
35 40 45
Ala Glu Tyr Met Val Asp Phe Leu Pro Lys Val Lys Ile Glu Ile Val
50 55 60
Val Thr Asp Asp Ile Val Asp Thr Cys Val Asp Thr Ile Ile Arg Thr
65 70 75 80
Ala Gln Thr Gly Lys Ile Gly Asp Gly Lys Ile Phe Val Phe Asp Val
85 90 95
Ala Arg Val Ile Arg Ile Arg Thr Gly Glu Glu Asp Asp Ala Ala Ile

100

105

110

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Lys Lys Ile Asp Ala Ile Ile Lys Pro Phe Lys Leu Asp Asp Val
1 5 10 15
Arg Glu Ala Leu Ala Glu Val Gly Ile Thr Gly Met Thr Val Thr Glu
20 25 30
Val Lys Gly Phe Gly Arg Gln Lys Gly His Thr Glu Leu Tyr Arg Gly
35 40 45
Ala Glu Tyr Met Val Asp Phe Leu Pro Lys Val Lys Ile Glu Ile Val
50 55 60
Val Pro Asp Asp Ile Val Asp Thr Cys Val Asp Thr Ile Ile Arg Thr
65 70 75 80
Ala Gln Thr Gly Lys Ile Gly Asp Gly Lys Ile Phe Val Phe Asp Val
85 90 95
Ala Arg Val Ile Arg Ile Arg Thr Gly Glu Glu Asp Asp Ala Ala Ile
100 105 110

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Lys Lys Ile Glu Ala Ile Ile Lys Pro Phe Lys Leu Asp Glu Val
1 5 10 15
Arg Ser Pro Ser Gly Val Gly Leu Gln Gly Ile Thr Val Thr Glu Ala
20 25 30
Lys Gly Phe Gly Arg Gln Lys Gly His Thr Glu Leu Tyr Arg Gly Ala
35 40 45
Glu Tyr Val Val Asp Phe Leu Pro Lys Val Lys Val Glu Val Val Leu
50 55 60
Ala Asp Glu Asn Ala Glu Ala Val Ile Glu Ala Ile Arg Lys Ala Ala
65 70 75 80
Gln Thr Gly Arg Ile Gly Asp Gly Lys Ile Phe Val Ser Asn Val Glu
85 90 95
Glu Val Ile Arg Ile Arg Thr Gly Glu Thr Gly Ile Asp Ala Ile
100 105 110

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Lys Lys Ile Glu Ala Ile Ile Lys Pro Phe Lys Leu Asp Glu Val
1 5 10 15
Arg Ser Leu Ser Gly Val Gly Leu Gln Gly Ile Thr Val Thr Glu Ala
20 25 30
Lys Gly Phe Gly Arg Gln Lys Gly His Thr Asp Leu Tyr Arg Gly Ala
35 40 45
Glu Tyr Ile Val Asp Phe Leu Pro Lys Val Lys Ile Glu Ile Val Ile
50 55 60
Gly Asp Asp Leu Val Glu Arg Ala Ile Asp Ala Ile Arg Arg Ala Ala
65 70 75 80
Gln Thr Gly Arg Ile Gly Asp Gly Lys Ile Phe Val Ser Asn Ile Glu
85 90 95
Glu Ala Ile Arg Ile Arg Thr Gly Glu Ser Gly Leu Asp Ala Ile
100 105 110

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Lys Lys Ile Glu Ala Ile Ile Lys Pro Phe Lys Leu Asp Glu Val
1 5 10 15
Lys Glu Ala Leu His Glu Val Gly Ile Lys Gly Ile Thr Val Thr Glu
20 25 30
Ala Lys Gly Phe Gly Arg Gln Lys Gly His Thr Glu Leu Tyr Arg Gly
35 40 45
Ala Glu Tyr Val Val Asp Phe Leu Pro Lys Val Lys Ile Glu Val Val
50 55 60
Met Glu Asp Ser Leu Val Glu Arg Ala Ile Glu Ala Ile Gln Gln Ala
65 70 75 80
Ala His Thr Gly Arg Ile Gly Asp Gly Lys Ile Phe Val Thr Pro Val
85 90 95
Glu Glu Val Val Arg Ile Arg Thr Gly Glu Lys Gly Gly Asp Ala Ile
100 105 110

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Lys Lys Val Glu Ala Ile Ile Lys Pro Phe Lys Leu Asp Glu Val
1 5 10 15
Lys Glu Ala Leu Gln Glu Ala Gly Ile Gln Gly Leu Ser Val Ile Glu
20 25 30
Val Lys Gly Phe Gly Arg Gln Lys Gly His Thr Glu Leu Tyr Arg Gly
35 40 45
Ala Glu Tyr Val Val Asp Phe Leu Pro Lys Val Lys Ile Glu Met Val
50 55 60
Leu Pro Asp Glu Met Val Asp Ile Ala Ile Glu Ala Ile Val Gly Ala
65 70 75 80
Ala Arg Thr Glu Lys Ile Gly Asp Gly Lys Ile Phe Val Ser Ser Ile
85 90 95
Glu Gln Ala Ile Arg Ile Arg Thr Gly Glu Thr Gly Glu Asp Ala Val

100

105

110

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Lys Lys Ile Glu Ala Ile Ile Arg Pro Phe Lys Leu Asp Glu Val
1 5 10 15
Lys Ile Ala Leu Val Asn Ala Gly Ile Val Gly Met Thr Val Ser Glu
20 25 30
Val Arg Gly Phe Gly Arg Gln Lys Gly Gln Thr Glu Arg Tyr Arg Gly
35 40 45
Ser Glu Tyr Thr Val Glu Phe Leu Gln Lys Leu Lys Leu Glu Ile Val
50 55 60
Val Glu Asp Ala Gln Val Asp Thr Val Ile Asp Lys Ile Val Ala Ala
65 70 75 80
Ala Arg Thr Gly Glu Ile Gly Asp Gly Lys Ile Phe Val Ser Pro Val
85 90 95
Asp Gln Thr Ile Arg Ile Arg Thr Gly Glu Lys Asn Ala Asp Ala Ile
100 105 110

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Lys Met Ile Lys Ala Ile Val Arg Pro Asp Lys Val Asp Asp Ile
1 5 10 15
Val Asp Ser Leu Glu Asn Ala Gly Tyr Pro Ala Phe Thr Lys Ile Asn
20 25 30
Ser Val Gly Arg Gly Lys Gln Gly Leu Lys Val Gly Glu Ile Phe
35 40 45
Tyr Asp Glu Leu Pro Lys Thr Ile Leu Ile Ala Val Asn Asp Asp
50 55 60
Glu Val Asp Glu Val Val Gly Leu Ile Lys Ser Ser Ala Ser Thr Gly
65 70 75 80
Asn Phe Gly Asp Gly Lys Ile Phe Ile Gln Pro Ile Thr Glu Ala Tyr
85 90 95
Thr Ile Arg Thr Gly Glu Thr Gly Ile
100 105

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Lys Glu Val Ile Ala Ile Ile Arg Pro Asn Thr Val Ser Lys Thr
 1 5 10 15
 Val Lys Ala Leu Asp Val Val Gly Phe Pro Ala Val Thr Met Ala Glu
 20 25 30
 Cys Phe Gly Arg Gly Lys Gln Lys Gly Tyr Glu Glu Gly Glu Lys Glu
 35 40 45
 Gly Arg Phe Ile Lys Tyr Ile Pro Lys Arg Leu Ile Ser Ile Val Val
 50 55 60
 Asp Asp Ala Asp Val Pro Leu Val Val Gly Ile Ile Ser Lys Val Asn
 65 70 75 80
 Arg Thr Gly Ser Phe Gly Asp Gly Arg Ile Phe Val Leu Pro Val Glu
 85 90 95
 Glu Ala Ile Arg Val Arg Thr Gly Glu Thr Gly Glu Ile Ala Ile
 100 105 110

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Phe Ser Ala Asn Leu Pro Glu Ile Val Asp Ile Gln Lys Ile Ile
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTGAAAGTTG	TGTTAAAAAA	AAAACTAGAA	TCATGGCGGC	GTCAATGACG	AAACCCATCT	60
CAATAACTTC	TCTCGGTTTC	TATTCTGATC	GAAAGAACAT	TGCTTCTCT	GATTGCATTT	120
CGATTGTTTC	TGGATTCAAGA	CATTCCCGAC	CATCTTGCC	CGATTGGTC	ACAAAGTCAC	180
CGAGTAATAA	CAGTCGTGTT	TTACCTGTCG	TTAGTGC	CCAAATCTCT	GATTATATT	240
CAGACTCGAA	ATTTTACAAG	GTGGAAGCAA	TTGTCAGACC	ATGGAGAATC	CAGCAAGTTT	300
CATCGGCTTT	ACTGAAAATC	GGGATTTCGAG	GTGTTACTGT	TTCCTGATGTG	AGAGGGTTG	360
GTGCACAAGG	AGGTTCTACC	GAGAGACACG	GTGGCTCTGA	GTTCTCGGAA	GACAAATTG	420
TTGCTAAAGT	TAAGATGGAA	ATCGTTGTTA	AGAAAGACCA	AGTGAATCT	GTAATCAACA	480
CAATAATTGA	AGGAGCAAGG	ACAGGAGAGA	TTGGTGTAGG	CAAGATTTT	TTTTGCCTG	540
TGTCAGATGT	CATAAGAGTT	AGGACAGGTG	AGCGTGGGGA	GAAAGCAGAG	AAGATGACTG	600
GTGATATGCT	TTCACCGTCT	TAGGAACAAA	CAGAGCTCAA	GAATGGTTT	TTTTTTTTC	660
ATTCGGTCT	CTAGATTCTG	CGAATAATAA	TGAATGGAGT	CTGTGTTGG	TTTCATGTTG	720
AATCGATCAA	GATGTGTTT	TAACTGTACA	TGAATTATGC	AGAAACATCT	GTCCTGGTTC	780
TCAGACATCG	AAACTCTGTT	CCTAATAAAA	AAAAAAA			817

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GC GG TG TC GG	CC GCT C TAG A	ACT AGT GG AT	CCC CCG GGC T	GC AGG AAT TC	GG CAC GAG GC	60
TA CT GC GAA A	CT GGG CT TG C	TC ACT CCT CT	TC ATT CT A AT	AA CAT CA AG A	A AGA ATT CCC	120
TG TTT TTG AT	TTC AG TTT GT	TTT GT CC AG A	GCT TAG AC AT	TCT CG GT TTT	CTC ACT TT A A	180
CA CCC CG GGT C	AAG CG CG TAA	GAT AT GCCC C	CGT CG TT CT	GTG AT TA AT G	CCC AA AG CT C	240
GC CT GACT AC	AT TCC CT GAT G	CT AA ATT CTA	CAA AGT GG AA	GCA ATT CT CA	GG CC CT GG CG	300
AGT CT CG CAA	GT T T CCG T C G	CT T T GCT AAA	AAT TGG T ATT	CG AGG GT GT TA	CT GTT T CT GA	360
TG TT CG AG GT	TTT GGT GCT C	AAG GT GG TT C	A CT GAG AG G	CAG GG CG GCT	CAG AAT T T C	420
TG A AGA CAA G	TTT GT TG CT A	AAG TT AAG AT	GG AGA T CG T G	GTT AG CAA AG	ACC AG GT T G A	480
GG AT GT TATA	GA AAA AA AT CA	TT GAG GAG G	AAG AACT G G A	GAG AT TGG AG	AC GG CA A G AT	540
TT T CT TG CT G	CCT GTT TC AG	AT GT A AT A A G	AGT CCG C A CT	GGT GAG C G G G	GT GATA AAG G C	600
TG AG AGG AT G	AC AGG AGG G G C	GAT CT GAC AT	GAG TACT T CT	GCT TG ACT G C	TGT GAC C A G C	660
AAT AT A GCA T	TC AGG ACT AA	CT GT C C T T T G	AG AA AG C C C C	GCC CTT AT TA	GCC ATT AT T C C	720
AG T AT A GCT T	GATA AT T T G A	AT T T T T G T T	TT CTT AACT A	AAG AA AC A A A	GAT CTT T C A	780
TT AT C CT G T T	GAT GATA AT T	GA AA AC CG G A A	GG AT CG CG A A	TTT GT T C A A G	TG CT TG C A A G	840
ATA A A A A A C A	AGA AGA GAG G A G	TA AT GT T A A C	AA A A A A A A A A A	AA A A A A A A A A A	ACT CG G A G	897

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AT GG CG GCG T	CA AT GAC GAA	ACCC AT CT CA	AT AA ACT TT CTC	TC GG TT T CTA	TT CT GAT CG A	60
AAG AAC AT TG	CT TT CT CT GA	TT GC AT TT CG	AT TT GTT CT G	GAT TC AG A CA	TT CCC GAC CA	120
TCT TGC CT CG	AT TT GG T C A C	AA AGT CAC CG	AG TA ATA A CA	GT CG GT TTT	AC CT GT CG TT	180
AGT G C C C A A A	TAT CT CT CT GA	TT AT AT T CCA	GA CT CG A A AT	TT T AC AAG GT	GG AAG CA A TT	240
GTC AG AC CAT	GG AGA AT CCA	GCA AG TT CCA	TC GG CT TT AC	TG AAA AT CG G	GAT TC GAG G T	300
GTT ACT GT T T	CT GAT GT GAG	AG GG GT TT GGT	GC AC AAG GAG	GTT CT ACC G A	GAG AC AC GG T	360
GG CT CT GAG T	TCT CG G A A G A	CAA AT TT G T T	GCT TAA AG T T A	AG AT GG A A AT	CG TT GT T A A G	420
AA AG ACC A A G	TG GA AT CT GT	AA T CA AC A C A	AT AA TT G A A G	GAG CA AG G A C	AG GAG AG A T T	480
GG T GAT GG C A	AG AT T T T T G T	TT G C T G T G	TC AG AT GT C A	TA AG AG T T A G	GAC AG GT GAG	540
CG T G G G G A G A	AA G C A G A G A A	GAT GACT G G T	GAT AT G C T T	CAC CG T C T		588

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 594 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CG CG CAC GAG G	CT ACT G C G A A	ACT GGG CTT G	CT C A C T C C T C	TTC ATT CT AA	TA AC AT CA A G	60
AA AG A A T T C C	CT GT T T T T G A	TT T C A G T T T G	TT T G T C C A G	AG CT T A G A C A	TT CT CG GT T T	120
TCT C A C T T A	AC ACC G C G G T	CA AG C G C G T A	AG AT AT G C C C	CC G T C G T T C C	TGT GAT TA A T	180
GCC C A A G C T	C G C C T G A C T A	C A T T C C T G A T	G C T A A A T T C T	A C A A A G T G G A	A G C A A T T C C	240
AG G C C T G G C	G A G T C T C G C A	A G T T C C T C G	G C T T G C T A A	A A A T T G G T A T	T C G A G G T G T T	300
A C T G T T C T G	A T G T T C G A G G	T T T T G G T G C T	C A A G G T G G T T	C A A C T G A G A G	G C A G G G C G G C	360
T C A G A A T T T T	C T G A A G A C A A	G T T T G G T G C T	A A A G T T A A G A	T G G A G A T C G T	G G T T A G C A A A	420
G A C C A G G T T G	A G G A T G T T A T	A G A A A A A T C	A T T G A G G A G G	C A A G A A C T G G	A G A G A T T G G A	480
G A C G G C A A G A	T T T T C T T G C T	G C C T G T T T C A	G A T G T A A T A A	G A G T C C G C A C	T G G T G A G C G G	540
G G T G A T A G G	C T G A G A G G G A T	G A C A G G G A G G G	C G A T C T G A C A	T G A G T A C T T C	T G C T	594

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCAAGATGGT CGGGAATGTC

20

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CGACAGGTAA AACACGACTG

20

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGTCTGACAA TTGCTTCCAC

20

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GAAACCAAAC ACAGACTCC

19

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCGAGTAATA ACAGTCGTC

19